

**Supplementary Figure 1:** Workflow of the FIE-FTICR MS-based platform for metabolomics. Plasma samples were first extracted and then directly injected into FTICR MS without LC separation for detection and label-free quantification of metabolite features. Metaboscape 4.0 was used for statistical analysis and SmartFormula annotation. METLIN annotation provided chemical names of putative metabolites by accurate mass matching.